

Figure 1-1

| EXON (SIZE)      | EXON 3'            | INTRON (SIZE)                          | EXON 5'                                    |
|------------------|--------------------|--|--|
| EXON 1 (>460 bp) | GCT G<br>Ala A     | gtgagtagctccggc... intron 1 (>30 kb)   | ..tttcctttatttttag<br>CT TCG<br>la Ser     |
| EXON 2 (171 bp)  | CAA G<br>Gln G     | gcaagtgtactttc... intron 2 (~2.3 kb)   | ..catattgatttttag<br>GA TAT<br>ly Cys      |
| EXON 3 (171 bp)  | CTC A<br>Leu S     | gtaagtaaaagtaacc... intron 3 (>30 kb)  | ..tttggttttcttttttag<br>GT CCA<br>er Pro   |
| EXON 4 (111 bp)  | ACA G<br>Thr G     | gtaaaaaattaccatt... intron 4 (~3.8 kb) | ..ttcctgttcttttag<br>GA GAC<br>ly Asp      |
| EXON 5 (92 bp)   | TTG GAG<br>Leu Glu | gtaagtttgccggtta... intron 5 (~6 kb)   | ..ttaaaacacacttgacag<br>CTG ATT<br>Leu Ile |
| EXON 6 (231 bp)  | CCC AAT<br>Pro Asn | gtaagttcttccatag... intron 6 (~4.1 kb) | ..tttctcctctatatag<br>GGA TCT<br>Gly Ser   |
| EXON 7 (115 bp)  | GGA G<br>Gly A     | gtaagatagtcata... intron 7 (>7 kb)     | ..aaattatccaaacag<br>AT CAT<br>sp His      |
| EXON 8 (161 bp)  | AGC GAG<br>Ser Glu | gtgagtgatatacaaa... intron 8 (~1.6 kb) | ..actctaattttatcag<br>GTT GGC<br>Val Gly   |
| EXON 9 (148 bp)  | CCA G<br>Pro G     | gtaaaaaactactgtc... intron 9 (>9.7 kb) | ..tctacaataatccacag<br>GG GAA<br>ly Glu    |
| EXON 10 (137 bp) | AGC CTG<br>Ser Leu | gtaagaaaaaaactaa... intron 10 (>5 kb)  | ..tactttgtctttacag<br>GCA GTG<br>Ala Val   |
| EXON 11 (173 bp) | GAA CG             | gtaagaccctaagg... intron 11 (>20 kb)   | ..ctttctttcttttaag<br>C AAC                |

Figure 1-2

|  | Glu Ar            |       |                  |                     |                    |        |        |
|--|-------------------|-------|------------------|---------------------|--------------------|--------|--------|
|  | EXON 12 (1280 bp) | CAG A | gtaaggaggagatc.. | intron 12 (~1.8 kb) | ..caacttttattttcag | TA GGT |        |
|  |                   | Gln I |                  |                     |                    |        | g Asn  |
|  | EXON 13 (>251 bp) |       |                  |                     |                    |        | le Gly |

**Figure 2**

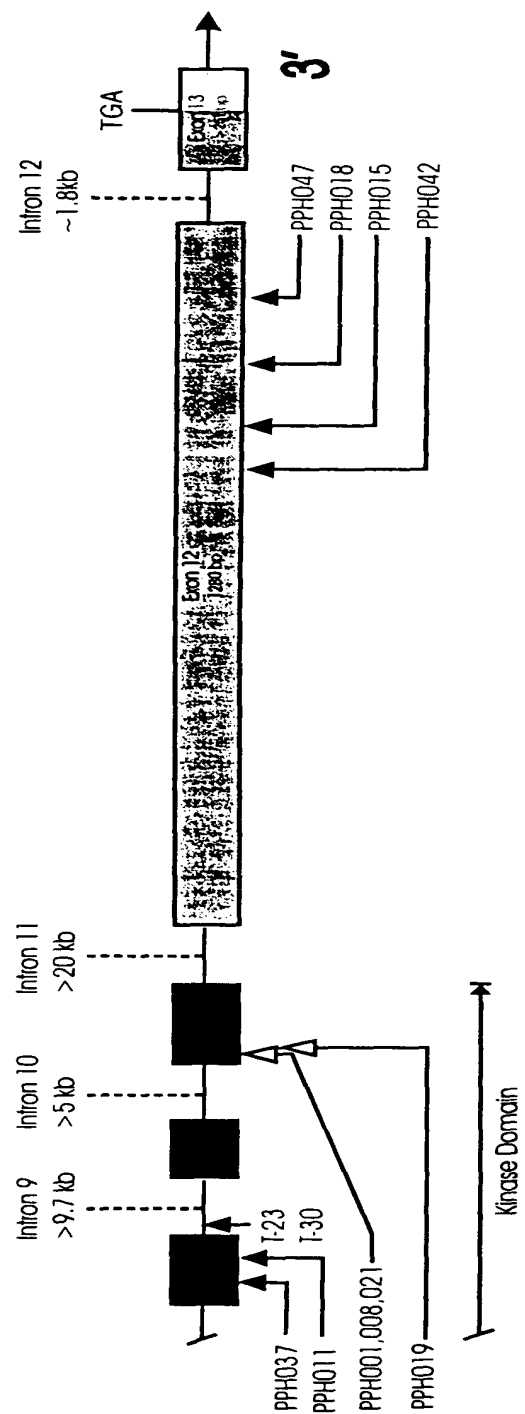
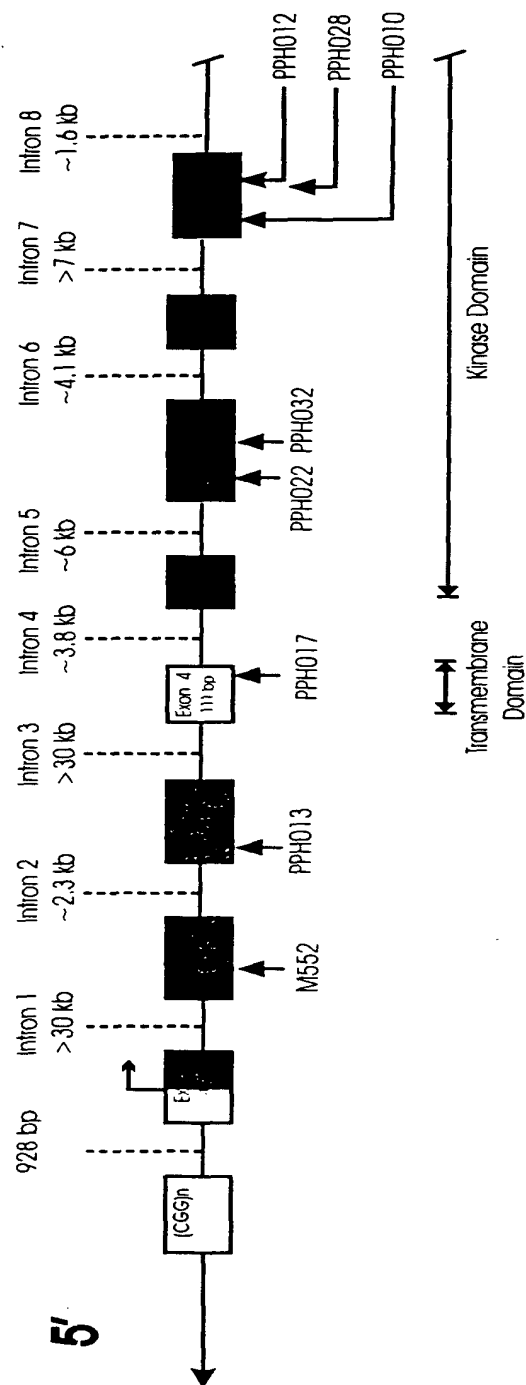


Figure 3

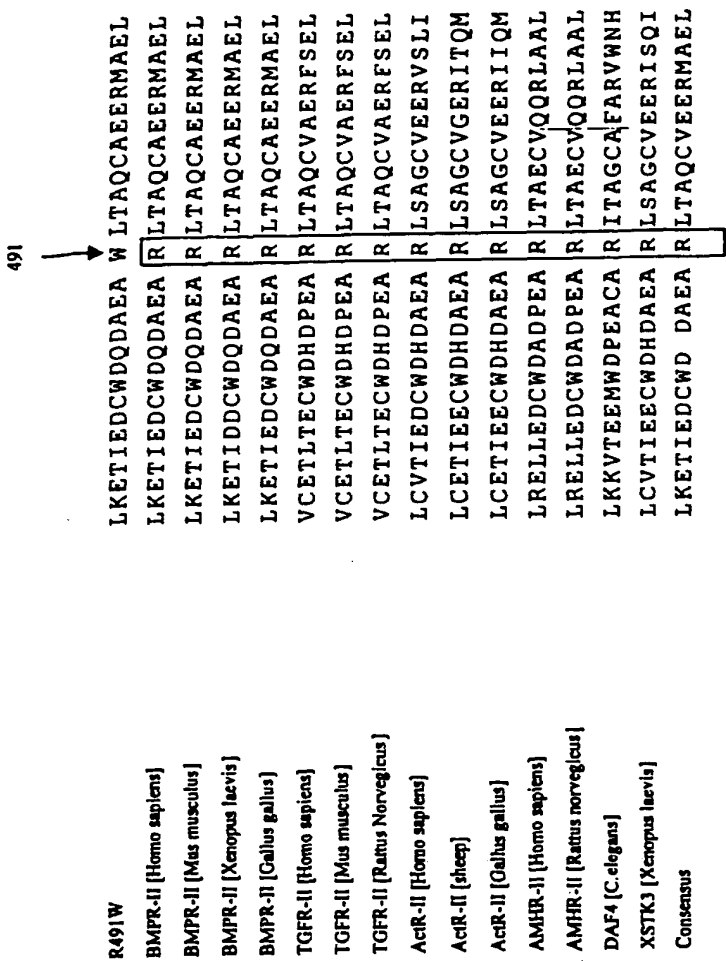


Figure 4

| Family #            | #A/#C/#U | Exon # | DNA Sequence Variation | Protein Sequence Variation |
|---------------------|----------|--------|------------------------|----------------------------|
| PPH001, 008 and 021 | 4/5/13   | 11     | 1471C>T                | R491W                      |
| PPH010              | 2/0/1    | 8      | 1099-1103delGGGA       | E368fsX1                   |
| PPH015              | 6/1/8    | 12     | 2579delT               | N861fsX10                  |
| PPH017              | 3/0/6    | 4      | 507-510delCTTTinsAAA   | C169X                      |
| PPH018              | 3/2/4    | 12     | 2617C>T                | R873X                      |
| PPH019              | 1/0/5*   | 11     | 1472G>A                | R491Q                      |
| PPH022              | 2/0/0    | 6      | 690-691delAGinsT       | K230fsX21                  |
| PPH011              |          | 9      | 1248-1251delATTT       | F417X                      |
| PPH012              |          | 8      | 994C>T                 | R332X                      |
| PPH013              |          | 3      | 295T>C                 | C99R                       |
| PPH028              |          | 8      | 1097delG               | P366fsX8                   |
| PPH032              |          | 6      | 727G>T                 | E243X                      |
| PPH037              |          | 9      | 1214delA               | D405fsX6                   |
| PPH042              |          | 12     | 2441-2442delAC         | H814fsX2                   |
| PPH047              |          | 12     | 2695C>T                | R899X                      |
| M552                |          | 2      | 189-209del21           | Del 64-70(STCYGLW)         |
| PPH045              |          | 3      | 296G>A                 | C99Y                       |
| PPH052              |          | 3      | 250T>C                 | C84R                       |
| PPH67-6701          |          | 8      | 1040G>A                | C347Y                      |

Figure 5-1

|     |             |            |            |             |            |            |            |             |            |            |     |     |     |     |     |     |     |
|-----|-------------|------------|------------|-------------|------------|------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|
| +1  | Met         | Thr        | Ser        | Ser         | Leu        | Gln        | Arg        | Pro         | Trp        | Arg        | Val | Pro | Trp | Leu | Pro | Trp | Thr |
| 1   | ATGACTTCCT  | CGCTGCAGCG | GCCCTGGCGG | GTGCCCTGGC  | TACCATGGAC | TACTGAAGGA | GCGACGTCGC | CGGGACCGCC  | CACGGGACCG | ATGGTACCTG |     |     |     |     |     |     |     |
| +1  | Thr         | Ile        | Leu        | Leu         | Val        | Ser        | Thr        | Ala         | Ala        | Ala        | Ser | Gln | Asn | Gln | Glu | Arg | Cys |
| 51  | CATCCTGCTG  | GTCAGCACTG | CGGCTGCTTC | GCAGAATCAA  | GAACGGCTAT | GTAGGACGAC | CAGTCGTGAC | GCCGACGAAG  | CGTCTTAGTT | CTTGCCGATA |     |     |     |     |     |     |     |
| +1  | Cys         | Ala        | Phe        | Lys         | Asp        | Pro        | Tyr        | Gln         | Gln        | Asp        | Leu | Gly | Ile | Gly | Glu | Ser | Arg |
| 101 | GTGCGTTTAA  | AGATCCGTAT | CAGCAAGACC | TTGGGATAGG  | TGAGAGTAGA | CACGCAAATT | TCTAGGCATA | GTGTTCTGG   | AACCTATCC  | ACTCTCATCT |     |     |     |     |     |     |     |
| +1  | Ile         | Ser        | His        | Glu         | Asn        | Gly        | Thr        | Ile         | Leu        | Cys        | Ser | Lys | Gly | Ser | Thr | Cys | Tyr |
| 151 | ATCTCTCATG  | AAAATGGGAC | AATATTATGC | TCGAAAGGTA  | GCACCTGCTA | TAGAGAGTAC | TTTTACCCTG | TTATAATACG  | AGCTTTCCAT | CGTGGACGAT |     |     |     |     |     |     |     |
| +1  | Tyr         | Gly        | Leu        | Trp         | Glu        | Lys        | Ser        | Lys         | Gly        | Asp        | Ile | Asn | Leu | Val | Lys | Gln | Gly |
| 201 | TGGCCTTTGG  | GAGAAATCAA | AAGGGGACAT | AAATCTTGTA  | AAACAAGGAT | ACCGGAAACC | CTCTTTAGTT | TTCCCCTGTA  | TTAGAACAT  | TTTGTTCCTA |     |     |     |     |     |     |     |
| +1  | Cys         | Trp        | Ser        | His         | Ile        | Gly        | Asp        | Pro         | Gln        | Glu        | Cys | His | Tyr | Glu | Glu | Cys | Val |
| 251 | GTTGGTCTCA  | CATTGGAGAT | CCCCAAGAGT | GTCACTATGA  | AGAATGTGTA | CAACCAGAGT | GTAACCTCTA | GGGGTTCTCA  | CAGTGATACT | TCTTACACAT |     |     |     |     |     |     |     |
| +1  | Val         | Thr        | Thr        | Thr         | Pro        | Pro        | Ser        | Ile         | Gln        | Asn        | Gly | Thr | Tyr | Arg | Phe | Cys | Cys |
| 301 | GTAAC TACCA | CTCCTCCCTC | AATTCAGAAT | GGAACATAACC | GTTTCTGCTG | CATTGATGGT | GAGGAGGGAG | TTAAGTCTTA  | CCTTGATATG | CAAAGACGAC |     |     |     |     |     |     |     |
| +1  | Cys         | Cys        | Ser        | Thr         | Asp        | Leu        | Cys        | Asn         | Val        | Asn        | Phe | Thr | Glu | Asn | Phe | Pro | Pro |
| 351 | TTGTAGCACA  | GATTTATGTA | ATGTCAACTT | TACTGAGAAT  | TTTCCACCTC | AACATCGTGT | CTAAATACAT | TACAGTTGAA  | ATGACTCTTA | AAAGGTGGAG |     |     |     |     |     |     |     |
| +1  | Pro         | Asp        | Thr        | Thr         | Pro        | Leu        | Ser        | Pro         | Pro        | His        | Ser | Phe | Asn | Arg | Asp | Glu | Thr |
| 401 | CTGACACAAC  | ACCACTCAGT | CCACCTCATT | CATTTAACCG  | AGATGAGACA | GACTGTGTTG | TGGTGAGTCA | GGTGGAGTAA  | GTAAATTGGC | TCTACTCTGT |     |     |     |     |     |     |     |
| +1  | Ile         | Ile        | Ile        | Ala         | Leu        | Ala        | Ser        | Val         | Ser        | Val        | Leu | Ala | Val | Leu | Ile | Val | Ala |
| 451 | ATAATCATTG  | CTTTGGCATC | AGTCTCTGTA | TTAGCTGTTT  | TGATAGTTGC | TATTAGTAAC | GAAACCGTAG | TCAGAGACAT  | AATCGACAAA | ACTATCAACG |     |     |     |     |     |     |     |
| +1  | Ala         | Leu        | Cys        | Phe         | Gly        | Tyr        | Arg        | Met         | Leu        | Thr        | Gly | Asp | Arg | Lys | Gln | Gly | Leu |
| 501 | CTTATGCTTT  | GGATACAGAA | TGTTGACAGG | AGACCGTAAA  | CAAGGTCTTC | GAATACGAAA | CCTATGTCTT | ACAACGTGCC  | TCTGGCATTT | GTTCCAGAAG |     |     |     |     |     |     |     |
| +1  | His         | Ser        | Met        | Asn         | Met        | Met        | Glu        | Ala         | Ala        | Ala        | Ser | Glu | Pro | Ser | Leu | Asp | Leu |
| 551 | ACAGTATGAA  | CATGATGGAG | GCAGCAGCAT | CCGAACCCCTC | TCTTGATCTA | TGTCATACTT | GTAACCTC   | CGTCGTCGTA  | GGCTTGGGAG | AGAAGTAGAT |     |     |     |     |     |     |     |
| +1  | Asp         | Asn        | Leu        | Lys         | Leu        | Leu        | Glu        | Leu         | Ile        | Gly        | Arg | Gly | Arg | Tyr | Gly | Ala | Val |
| 601 | GATAATCTGA  | AACTGTTGGA | GCTGATTGGC | CGAGGTCGAT  | ATGGAGCAGT | CTATTAGACT | TTGACAACCT | CGACTAACCG  | GCTCCAGCTA | TACCTCGTCA |     |     |     |     |     |     |     |
| +1  | Val         | Tyr        | Lys        | Gly         | Ser        | Leu        | Asp        | Glu         | Arg        | Pro        | Val | Ala | Val | Lys | Val | Phe | Ser |
| 651 | ATATAAAGGC  | TCCTTGATG  | AGCGTCCAGT | TGCTGTAAAA  | GTGTTTTCTT | TATATTTCCG | AGGAACCTAC | TCGCAGGTCA  | ACGACATTTT | CACAAAAGGA |     |     |     |     |     |     |     |
| +1  | Phe         | Ala        | Asn        | Arg         | Gln        | Asn        | Phe        | Ile         | Asn        | Glu        | Lys | Asn | Ile | Tyr | Arg | Val | Pro |
| 701 | TTGCAAACCG  | TCAGAATTTT | ATCAACGAAA | AGAACATTTA  | CAGAGTGCTT | AACGTTTGGC | AGTCTTAAAA | TAGTTGCTTT  | TCTTGTAAT  | GTCTCACGGA |     |     |     |     |     |     |     |
| +1  | Leu         | Met        | Glu        | His         | Asp        | Asn        | Ile        | Ala         | Arg        | Phe        | Ile | Val | Gly | Asp | Glu | Arg | Val |
| 751 | TTGATGGAAC  | ATGACAACAT | TGCCCGCTTT | ATAGTTGGAG  | ATGAGAGAGT | AACTACCTTG | TACTGTTGTA | ACGGGGCGAAA | TATCAACCTC | TACTCTCTCA |     |     |     |     |     |     |     |

## Figure 5-2

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+1 Val Thr Ala Asp Gly Arg Met Glu Tyr Leu Leu Val Met Glu Tyr Tyr Pro Asn
801 CACTGCAGAT GGACGCATGG AATATTTGCT TGTGATGGAG TACTATCCCA
GTGACGTCTA CCTGCGTACC TTATAAACGA ACACTACCTC ATGATAGGGT
+1 Asn Gly Ser Leu Ofs Lys Tyr Leu Ser Leu His Thr Ser Asp Trp Val Ser
851 ATGGATCTTT ATGCAAGTAT TTAAGTCTCC ACACAAGTGA CTGGGTAAGC
TACCTAGAAA TACGTTTCATA AATTCAGAGG TGTGTTCACT GACCCATTCTG
+1 Ser Ofs Arg Leu Ala His Ser Val Thr Arg Gly Leu Ala Tyr Leu His Thr
901 TCTTGCCGTC TTGCTCATTC TGTTACTAGA GGACTGGCTT ATCTTCACAC
AGAACGGCAG AACGAGTAAG ACAATGATCT CCTGACCGAA TAGAAGTGTG
+1 Thr Glu Leu Pro Arg Gly Asp His Tyr Lys Pro Ala Ile Ser His Arg Asp Leu
951 AGAATTACCA CGAGGAGATC ATTATAAACC TGCAATTTCC CATCGAGATT
TCTTAATGGT GCTCCTCTAG TAATATTTGG ACGTTAAAGG GTAGCTCTAA
+1 Leu Asn Ser Arg Asn Val Leu Val Lys Asn Asp Gly Thr Ofs Val Ile Ser
1001 TAAACAGCAG AAATGTCCTA GTGAAAAATG ATGGAACCTG TGTATTAGT
ATTTGTCGTC TTACAGGAT CACTTTTTAC TACCTTGGAC ACAATAATCA
+1 Asp Phe Gly Leu Ser Met Arg Leu Thr Gly Asn Arg Leu Val Arg Pro Gly
1051 GACTTTGGAC TGTCCATGAG GCTGACTGGA AATAGACTGG TCGCGCCAGG
CTGAAACCTG ACAGGTAATC CGACTGACCT TTATCTGACC ACGCGGGTCC
+1 Gly Glu Glu Asp Asn Ala Ala Ile Ser Glu Val Gly Thr Ile Arg Tyr Met Ala
1101 GGAGGAAGAT AATGCAGCCA TAAGCGAGGT TGGCACTATC AGATATATGG
CCTCCTTCTA TTACGTCGGT ATTCGCTCCA ACCGTGATAG TCTATATACC
+1 Ala Pro Glu Val Leu Glu Gly Ala Val Asn Leu Arg Asp Ofs Glu Ser Ala
1151 CACCAGAAGT GCTAGAAGGA GCTGTGAACT TGAGGGACTG TGAATCAGCT
GTGGTCTTCA CGATCTTCCT CGACACTTGA ACTCCCTGAC ACTTAGTCGA
+1 Leu Lys Gln Val Asp Met Tyr Ala Leu Gly Leu Ile Tyr Trp Glu Ile Phe
1201 TTGAAACAAG TAGCATGTA TGCTCTTGGA CTAATCTATT GGGAGATATT
AACTTTGTTT ATCTGTACAT ACGAGAACCT GATTAGATAA CCCTCTATAA
+1 Phe Met Arg Ofs Thr Asp Leu Phe Pro Gly Glu Ser Val Pro Glu Tyr Gln Met
1251 TATGAGATGT ACAGACCTCT TCCCAGGGGA ATCCGTACCA GAGTACCAGA
ATACTCTACA TGTCTGGAGA AGGGTCCCT TAGGCATGGT CTCATGGTCT
+1 Met Ala Phe Gln Thr Glu Val Gly Asn His Pro Thr Phe Glu Asp Met Gln
1301 TGGCTTTTCA GACAGAGGTT GGAAACCATC CCACTTTTGA GGATATGCAG
ACCGAAAAGT CTGTCTCCAA CCTTTGGTAG GGTGAAAACCT CCTATACGTC
+1 Val Leu Val Ser Arg Glu Lys Gln Arg Pro Lys Phe Pro Glu Ala Trp Lys
1351 GTTCTCGTGT CTAGGGAAAA ACAGAGACCC AAGTTCCAG AAGCCTGGAA
CAAGAGCACA GATCCCTTTT TGTCTCTGGG TTCAAGGGTC TTCGGACCTT
+1 Lys Glu Asn Ser Leu Ala Val Arg Ser Leu Lys Glu Thr Ile Glu Asp Ofs Trp
1401 AGAAAATAGC CTGGCAGTGA GGTCACTCAA GGAGACAATC GAAGACTGTT
TCTTTTATCG GACCGTCACT CCAGTGAGTT CCTCTGTTAG CTCTGACAA
+1 Trp Asp Gln Asp Ala Glu Ala Arg Leu Thr Ala Gln Ofs Ala Glu Glu Arg
1451 GGGACCAGGA TGCAGAGGCT CGGCTTACTG CACAGTGTGC TGAGGAAAGG
CCCTGGTCTT ACGTCTCCGA GCCGAATGAC GTGTCACACG ACTCCTTTCC
+1 Met Ala Glu Leu Met Met Ile Trp Glu Arg Asn Lys Ser Val Ser Pro Thr
1501 ATGGCTGAAC TTATGATGAT TTGGGAAAGA AACAAATCTG TGAGCCCAAC
TACCGACTTG AATACTACTA AACCTTTTCT TTGTTTAGAC ACTCGGGTTG
+1 Thr Val Asn Pro Met Ser Thr Ala Met Gln Asn Glu Arg Asn Leu Ser His Asn
1551 AGTCAATCCA ATGTCTACTG CTATGCAGAA TGAACGCAAC CTGTCACATA
TCAGTTAGGT TACAGATGAC GATACGTCTT ACTTGCGTTG GACAGTGTAT

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Figure 5-3

|      |            |             |            |             |            |            |             |            |            |             |     |     |     |     |     |     |     |
|------|------------|-------------|------------|-------------|------------|------------|-------------|------------|------------|-------------|-----|-----|-----|-----|-----|-----|-----|
| +1   | Asn        | Arg         | Arg        | Val         | Pro        | Lys        | Ile         | Gly        | Pro        | Tyr         | Pro | Asp | Tyr | Ser | Ser | Ser | Ser |
| 1601 | ATAGGCGTGT | GCCAAAAATT  | GGTCCTTATC | CAGATTATTC  | TTCCTCCTCA | TATCCGCACA | CGGTTTTTAA  | CCAGGAATAG | GTCTAATAAG | AAGGAGGAGT  |     |     |     |     |     |     |     |
| +1   | Tyr        | Ile         | Glu        | Asp         | Ser        | Ile        | His         | His        | Thr        | Asp         | Ser | Ile | Val | Lys | Asn | Ile | Ser |
| 1651 | TACATTGAAG | ACTCTATCCA  | TCATACTGAC | AGCATCGTGA  | AGAATATTTC | ATGTAACCTC | TGAGATAGGT  | AGTATGACTG | TCGTAGCACT | TCTTATAAAG  |     |     |     |     |     |     |     |
| +1   | Ser        | Ser         | Glu        | His         | Ser        | Met        | Ser         | Ser        | Thr        | Pro         | Leu | Thr | Ile | Gly | Glu | Lys | Asn |
| 1701 | CTCTGAGCAT | TCTATGTCCA  | GCACACCTTT | GACTATAGGG  | GAAAAAAACC | GAGACTCGTA | AGATACAGGT  | CGTGTGGAAA | CTGATATCCC | CTTTTTTTGG  |     |     |     |     |     |     |     |
| +1   | Arg        | Asn         | Ser        | Ile         | Asn        | Tyr        | Glu         | Arg        | Gln        | Gln         | Ala | Gln | Ala | Arg | Ile | Pro | Ser |
| 1751 | GAAATTCAAT | TAACTATGAA  | CGACAGCAAG | CACAAGCTCG  | AATCCCCAGC | CTTTAAGTTA | ATTGATACTT  | GCTGTCGTTC | GTGTTCGAGC | TTAGGGGTCTG |     |     |     |     |     |     |     |
| +1   | Pro        | Glu         | Thr        | Ser         | Val        | Thr        | Ser         | Leu        | Ser        | Thr         | Asn | Thr | Thr | Thr | Thr | Asn | Thr |
| 1801 | CCTGAAACAA | GTGTCAACCAG | CCTCTCCACC | AACACAACAA  | CCACAAACAC | GGACTTTGTT | CACAGTGGTC  | GGAGAGGTGG | TTGTGTTGTT | GGTGTGTTGTG |     |     |     |     |     |     |     |
| +1   | Thr        | Thr         | Gly        | Leu         | Thr        | Pro        | Ser         | Thr        | Gly        | Met         | Thr | Thr | Ile | Ser | Glu | Met | Pro |
| 1851 | CACAGGACTC | ACGCCAAGTA  | CTGGCATGAC | TACTATATCT  | GAGATGCCAT | GTGTCTGAG  | TGCGGTTTCAT | GACCGTACTG | ATGATATAGA | CTCTACGGTA  |     |     |     |     |     |     |     |
| +1   | Tyr        | Pro         | Asp        | Glu         | Thr        | Asn        | Leu         | His        | Thr        | Thr         | Asn | Val | Ala | Gln | Ser | Ile | Gly |
| 1901 | ACCCAGATGA | AACAAATCTG  | CATACCACAA | ATGTTGCACA  | GTCAATTGGG | TGGGTCTACT | TTGTTTAGAC  | GTATGGTGTT | TACAACGTGT | CAGTTAACCC  |     |     |     |     |     |     |     |
| +1   | Pro        | Thr         | Pro        | Val         | Qys        | Leu        | Gln         | Leu        | Thr        | Glu         | Glu | Asp | Leu | Glu | Thr | Asn | Lys |
| 1951 | CCAACCCCTG | TCTGCTTACA  | GCTGACAGAA | GAAGACTTGG  | AAACCAACAA | GGTTGGGGAC | AGACGAATGT  | CGACTGTCTT | CTCTGAACC  | TTTGTTGTT   |     |     |     |     |     |     |     |
| +1   | Lys        | Leu         | Asp        | Pro         | Lys        | Glu        | Val         | Asp        | Lys        | Asn         | Leu | Lys | Glu | Ser | Ser | Asp | Glu |
| 2001 | GCTAGACCCA | AAAGAAGTTG  | ATAAGAACCT | CAAGGAAAGC  | TCTGATGAGA | CGATCTGGGT | TTTCTTCAAC  | TATTCTTGGA | GTTCTTTTCG | AGACTACTCT  |     |     |     |     |     |     |     |
| +1   | Asn        | Leu         | Met        | Glu         | His        | Ser        | Leu         | Lys        | Gln        | Phe         | Ser | Gly | Pro | Asp | Pro | Leu | Ser |
| 2051 | ATCTCATGGA | GCACTCTCTT  | AAACAGTTCA | GTGGCCCCAGA | CCCACTGAGC | TAGAGTACCT | CGTGAGAGAA  | TTTGTCAAGT | CACCGGTCT  | GGGTGACTCG  |     |     |     |     |     |     |     |
| +1   | Ser        | Thr         | Ser        | Ser         | Ser        | Leu        | Leu         | Tyr        | Pro        | Leu         | Ile | Lys | Leu | Ala | Val | Glu | Ala |
| 2101 | AGTACTAGTT | CTAGCTTGCT  | TTACCCACTC | ATAAACTTG   | CAGTAGAAGC | TCATGATCAA | GATCGAACGA  | AATGGGTGAG | TATTTTGAAC | GTCATCTTCG  |     |     |     |     |     |     |     |
| +1   | Ala        | Thr         | Gly        | Gln         | Gln        | Asp        | Phe         | Thr        | Gln        | Thr         | Ala | Asn | Gly | Gln | Ala | Qys | Leu |
| 2151 | AACTGGACAG | CAGGACTTCA  | CACAGACTGC | AAATGGCCAA  | GCATGTTTGA | TTGACCTGTC | GTCTGAAGT   | GTGCTGACG  | TTTACCGGTT | CGTACAAACT  |     |     |     |     |     |     |     |
| +1   | Ile        | Pro         | Asp        | Val         | Leu        | Pro        | Thr         | Gln        | Ile        | Tyr         | Pro | Leu | Pro | Lys | Gln | Gln | Asn |
| 2201 | TTCCTGATGT | TCTGCCTACT  | CAGATCTATC | CTCTCCCCAA  | GCAGCAGAAC | AAGGACTACA | AGACGGATGA  | GTCTAGATAG | GAGAGGGGTT | CGTCGTCTTG  |     |     |     |     |     |     |     |
| +1   | Leu        | Pro         | Lys        | Arg         | Pro        | Thr        | Ser         | Leu        | Pro        | Leu         | Asn | Thr | Lys | Asn | Ser | Thr | Lys |
| 2251 | CTTCCCAAGA | GACCTACTAG  | TTTGCCTTTG | AACACCAAAA  | ATTCAACAAA | GAAGGGTTCT | CTGGATGATC  | AAACGGAAAC | TTGTGGTTTT | TAAGTTGTTT  |     |     |     |     |     |     |     |
| +1   | Lys        | Glu         | Pro        | Arg         | Leu        | Lys        | Phe         | Gly        | Ser        | Lys         | His | Lys | Ser | Asn | Leu | Lys | Gln |
| 2301 | AGAGCCCCGG | CTAAAAATTG  | GCAGCAAGCA | CAAATCAAAC  | TTGAAACAAG | TCTCGGGGCC | GATTTTAAAC  | CGTCGTTTCG | GTTTAGTTTG | AACTTTGTTC  |     |     |     |     |     |     |     |
| +1   | Val        | Glu         | Thr        | Gly         | Val        | Ala        | Lys         | Met        | Asn        | Thr         | Ile | Asn | Ala | Ala | Glu | Pro | His |
| 2351 | TCGAAACTGG | AGTTGCCAAG  | ATGAATACAA | TCAATGCAGC  | AGAACCTCAT | AGCTTTGACC | TCAACGGTTC  | TACTTATGTT | AGTTACGTCG | TCTTGGAGTA  |     |     |     |     |     |     |     |



[illegible]